



Supplementary Figure S1. Schistosome egg production is unaffected by decitabine (DAC). Schistosome adult worm pairs were cultivated with DAC (491 µM), 5-AzaC (491 µM) or media only (control). Egg production was quantified at 48 hr according to the Methods Section. Histograms represent mean (+ SEM) egg output derived from 5 worm pairs (n=10) cultured for 48 hr. A One-Way Analysis of Variance (ANOVA) followed by *post hoc* testing with Fisher's Least Significant Difference (LSD) was used to detect statistical differences (* represents $p < 0.05$, ns – not significant) in egg production amongst groups (Control, 491 µM 5-AzaC and 491 µM DAC).

Supplementary Table S1. *Schistosoma mansoni* DNA methylation machinery components

Gene name	NCBI ID	SchistoGeneDB ID	Top BLASTp Hit	Size (Bp)	Size (Aa)
SmDnmt2 isoform 1	HM991456	Smp_145390	NP_001156357	1107	369
SmDnmt2 isoform 2	HM991457	Smp_145390	CAF91437	1083	361
SmMBD	HM991455	Smp_138180	NP_001108497	945	315

Supplementary Table S2. *Schistosoma mansoni* Dnmt2 homologs

Organism	NCBI BLASTp ID	Percent AA Identity	E value
<i>Dictyostelium discoideum</i>	EAL63449	35	1E-50
<i>Drosophila melanogaster</i>	ABI31309	36	4E-55
<i>Entamoeba histolytica</i>	AAS66974	27	2E-29
<i>Homo sapiens</i>	AAC53529	39	7E-70
<i>Mus musculus</i>	AAC53529	39	5E-64
<i>Pristionchus pacificus</i>	AAV85978	33	1E-46
<i>Schizosaccharomyces pombe</i>	NP_595687	34	1E-47

The full length SmDnmt2 ORF (derived from HM991456) was subjected to BLASTp analysis. This table includes percent similarities and E values of homologous Dnmt2 proteins identified from seven different organisms contained in the NCBI databases.

Supplementary Table S3. *Schistosoma mansoni* MBD homologs

Organism	NCBI BLASTp ID	Percent AA Identity	E value
<i>Dictyostelium discoideum</i>	*	-	-
<i>Drosophila melanogaster</i>	AAF54400	36	2E-14
<i>Entamoeba histolytica</i>	*	-	-
<i>Homo sapiens</i>	AAC68871	40	1E-36
<i>Mus musculus</i>	AAC68872	40	4E-36
<i>Pristionchus pacificus</i>	AAV85979	30	4E-08
<i>Schizosaccharomyces pombe</i>	*	-	-

The full length SmMBD ORF (derived from HM991455) was subjected to BLASTp analysis. This table includes percent similarities and E values of homologous MBD proteins identified from four different organisms contained in the NCBI databases. * represents organisms that do not contain a MBD homolog (E value greater than 1E-05).

Supplementary Table S4. PCR primer sequences used in this study.

Amplified DNA element	Forward Primer Sequence (5'-3')	Reverse Primer Sequence (5'-3')	Amplicon size
SmDnmt2 (qRT-PCR)	CGTGTATCGAGAGTTTATGTC	TAATAAGCATTCTGAAACCAG	172bp
SmMBD (qRT-PCR)	CGGTTATTGTACGTTCTCATCC	CAGCACTCTGTATTCCTTTAGGC	129bp
SmAt1 (qRT-PCR)	CTTCGAACCAGCAAATCAGA	GACACCAATCCACAAACTGG	158bp
SmVal2 (gDNA)	TAAGAACTGATAATATACGC	GTTGTAGGGTGCAATTTATC	291bp
Mm Catalase (gDNA)	ATGGCCTCCGAGATCTTTTC	GGGTCAAAGCCATCTGTTC	653bp
Smp121930 (control PCR)	CAATATGGGCTTCAGAATAAAG	CGATACATTCACAGAAGTTTATTT	741bp
Smp121930 (control bisulfite PCR)	TATTGGTATTTTTTAGGAATGATG	ATCCAAAACCAATAACAAAAA	386bp
JF781495 (bisulfite PCR)	ATTGTGTAAGTGTTTAAATAAGTT	TGTTATTTAAGGAGTATAATTTAGTGAA	199bp